

SCORE Search Results Details for Application 10527708 and Search Result 20071114_121652_us-10-527-708-1.ra1.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10527708 and Search Result 20071114_121652_us-10-527-708-1.ra1.

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GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 14, 2007, 13:32:01 ; Search time 175 Seconds
(without alignments)
292.102 Million cell updates/sec

Title: US-10-527-708-1
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 983262 seqs, 142787483 residues

Total number of hits satisfying chosen parameters: 983262

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result	Query

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2	1891	100.0	358	3	US-10-462-072-1	Sequence 1, Appli
3	1887	99.8	358	2	US-09-909-474D-2	Sequence 2, Appli
4	1887	99.8	358	3	US-10-117-766A-2	Sequence 2, Appli
5	1884	99.6	358	2	US-09-909-474D-8	Sequence 8, Appli
6	1884	99.6	358	3	US-10-117-766A-8	Sequence 8, Appli
7	1874	99.1	360	3	US-10-117-766A-30	Sequence 30, Appl
8	1679	88.8	360	2	US-09-509-902A-9	Sequence 9, Appli
9	1679	88.8	360	2	US-10-024-828-9	Sequence 9, Appli
10	1679	88.8	360	2	US-09-909-474D-11	Sequence 11, Appl
11	1679	88.8	360	3	US-10-117-766A-11	Sequence 11, Appl
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16	1060	56.1	308	3	US-10-462-072-3	Sequence 3, Appli
17	752	39.8	343	3	US-10-462-072-8	Sequence 8, Appli
18	750.5	39.7	343	3	US-10-117-766A-32	Sequence 32, Appl
19	740.5	39.2	372	3	US-10-117-766A-33	Sequence 33, Appl
20	725.5	38.4	372	3	US-10-462-072-7	Sequence 7, Appli
21	564.5	29.9	214	3	US-10-462-072-4	Sequence 4, Appli
22	526.5	27.8	177	3	US-10-462-072-5	Sequence 5, Appli
23	433	22.9	484	3	US-10-117-766A-34	Sequence 34, Appl
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31	297.5	15.7	778	2	US-10-116-326-2	Sequence 2, Appli
32	297.5	15.7	778	2	US-10-003-690-2	Sequence 2, Appli
33	297.5	15.7	778	2	US-10-803-277-2	Sequence 2, Appli
34	292.5	15.5	607	1	US-08-878-989-15	Sequence 15, Appl
35	292.5	15.5	607	2	US-09-272-796-15	Sequence 15, Appl
36	288.5	15.3	523	3	US-10-183-687-258	Sequence 258, App
37	287	15.2	1518	2	US-09-487-558B-152	Sequence 152, App
38	285	15.1	512	2	US-09-633-328B-2	Sequence 2, Appli
39	284	15.0	504	3	US-10-183-687-407	Sequence 407, App
40	283.5	15.0	651	2	US-09-870-937-10	Sequence 10, Appl
41	283.5	15.0	651	3	US-10-173-999-127	Sequence 127, App
42	283	15.0	438	3	US-10-183-687-250	Sequence 250, App
43	278	14.7	570	3	US-10-183-687-240	Sequence 240, App
44	277	14.6	441	3	US-10-183-687-406	Sequence 406, App
45	277	14.6	511	2	US-09-633-328B-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-799-875-8

; Sequence 8, Application US/09799875

; Patent No. 6638721

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses

; TITLE OF INVENTION: Therefor
 ; FILE REFERENCE: 35800/209996
 ; CURRENT APPLICATION NUMBER: US/09/799,875
 ; CURRENT FILING DATE: 2001-03-06
 ; PRIOR APPLICATION NUMBER: 60/182,059
 ; PRIOR FILING DATE: 2000-02-11
 ; PRIOR APPLICATION NUMBER: 09/659,287
 ; PRIOR FILING DATE: 2000-09-12
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 8
 ; LENGTH: 358
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
US-09-799-875-8

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 Best Local Similarity 100.0%; Pred. No. 1.2e-185;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

US-10-462-072-1

; Sequence 1, Application US/10462072
 ; Patent No. 7220539
 ; GENERAL INFORMATION:
 ; APPLICANT: DU, KEYONG
 ; APPLICANT: HERZIG, STEPHAN
 ; APPLICANT: MONTMINY, MARC
 ; TITLE OF INVENTION: PROTEIN KINASE B/AKT MODULATORS AND METHODS FOR THE USE
 ; TITLE OF INVENTION: THEREOF
 ; FILE REFERENCE: SALK3120-1
 ; CURRENT APPLICATION NUMBER: US/10/462,072
 ; CURRENT FILING DATE: 2003-06-12
 ; PRIOR APPLICATION NUMBER: 60/388,508
 ; PRIOR FILING DATE: 2002-06-12
 ; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-462-072-1

Query Match 100.0%; Score 1891; DB 3; Length 358;
Best Local Similarity 100.0%; Pred. No. 1.2e-185;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-909-474D-2
; Sequence 2, Application US/09909474D
; Patent No. 6881542
; GENERAL INFORMATION:
; APPLICANT: Boylan, John
; APPLICANT: Bowers, Alex
; TITLE OF INVENTION: No. 6881542e1 Serine Threonine Kinase Member, h2520-59
; FILE REFERENCE: 01017/36524A
; CURRENT APPLICATION NUMBER: US/09/909,474D
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/219,204
; PRIOR FILING DATE: 2000-07-19
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 358
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-909-474D-2

Query Match 99.8%; Score 1887; DB 2; Length 358;
Best Local Similarity 99.7%; Pred. No. 3.1e-185;
Matches 357; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

SCORE Search Results Details for Application 10527708 and Search Result 20071114_121807_us-10-527-708-1.p2n.rni.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10527708 and Search Result 20071114_121807_us-10-527-708-1.p2n.rni.

[Go Back to previous](#)

GenCore version 6.2.1
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OM protein - nucleic search, using frame_plus_p2n model

Run on: November 14, 2007, 15:10:30 ; Search time 1030 Seconds
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Perfect score: 1891
Sequence: 1 MRATPLAAPAGSLSRKKRLE.....GLGLDEAREEEGDREVVLYG 358

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Listing first 4515 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1887	99.8	2059	5	US-10-117-766A-1
5	1686	89.2	1085	3	US-09-509-902A-3
6	1686	89.2	1085	3	US-10-024-828-3
7	862	45.6	510	3	US-09-909-474D-12
8	862	45.6	510	5	US-10-117-766A-12
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; Sequence 9, Application US/09799875
; Patent No. 6638721
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Williamson, Mark
; TITLE OF INVENTION: No. 6638721el Human Protein Kinases and Uses
; TITLE OF INVENTION: Therefor
; FILE REFERENCE: 35800/209996
; CURRENT APPLICATION NUMBER: US/09/799,875
; CURRENT FILING DATE: 2001-03-06
; PRIOR APPLICATION NUMBER: 60/182,059
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: 09/659,287
; PRIOR FILING DATE: 2000-09-12
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-799-875-9

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Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
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Qy    121 AlaArgProThrGluValLeuAlaGlyThrGlnLeuLeuTyrAlaPhePheThrArgThr 140
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Qy      301 AlaGluArgLeuThrAlaThrGlyIleLeuLeuHisProTrpLeuArgGlnAspProMet 320
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Db      901 GCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATG 960
Qy      321 ProLeuAlaProThrArgSerHisLeuTrpGluAlaAlaGlnValValProAspGlyLeu 340
      |||
Db      961 CCCTTAGCTCCAACCCGATCCCATCTCTGGGAGGCTGCCAGGTGGTCCCTGATGGACTG 1020
Qy      341 GlyLeuAspGluAlaArgGluGluGluGlyAspArgGluValValLeuTyrGly 358
      |||
Db      1021 GGGCTGGACGAAGCCAGGGAAGAGGAGGGAGACAGAGAAGTGTTCTGTATGGC 1074
<!--EndFragment-->
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<!--StartFragment-->RESULT 3

AAS06709

ID AAS06709 standard; cDNA; 1077 BP.

XX

AC AAS06709;

XX

DT 12-SEP-2001 (first entry)

XX

DE Polynucleotide sequence encoding human protein kinase #9.

XX

KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;

KW metabolic disorder; immune related disease; neurological disorder;

KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW reproductive disorder; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200138503-A2.

XX

PD 31-MAY-2001.

XX

PF 22-NOV-2000; 2000WO-US032085.

XX

PR 24-NOV-1999; 99US-0167482P.

XX

PA (SUGE-) SUGEN INC.

XX

PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI Flanagan P, Clary D;

XX

DR WPI; 2001-343950/36.

DR P-PSDB; AAU03509.

XX

PT Nucleic acids encoding human kinase polypeptides, useful for preventing
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
PT neuronal-associated diseases, and microbial infections.

XX

PS Example 1; Fig 1; 433pp; English.

XX

CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel
CC protein kinases have been identified as members of the tyrosine or
CC serine/threonine kinase (PTK and STK) families. The polynucleotides
CC encoding protein kinases and the polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate kinase expression. For example, they may be used to treat
CC cancers (especially cancers of haematopoietic origin), cardiovascular
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
CC immune related diseases (e.g. rheumatoid arthritis), neurological
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC Additionally, polynucleotides encoding protein kinases may be used for
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
CC polypeptides may be used as antigens in the production of antibodies
CC against the protein kinases and in assays to identify modulators of
CC protein kinase expression and activity

XX

SQ Sequence 1077 BP; 174 A; 373 C; 325 G; 205 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4.14e-122 Length: 1077

Score:	1891.00	Matches:	358
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	4	Gaps:	0

US-10-527-708-1 (1-358) x AAS06709 (1-1077)

Qy	1	MetArgAlaThrProLeuAlaAlaProAlaGlySerLeuSerArgLysLysArgLeuGlu	20
Db	1	ATGCGAGCCACCCCTCTGGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAG	60
Qy	21	LeuAspAspAsnLeuAspThrGluArgProValGlnLysArgAlaArgSerGlyProGln	40
Db	61	TTGGATGACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAG	120
Qy	41	ProArgLeuProProCysLeuLeuProLeuSerProProThrAlaProAspArgAlaThr	60
Db	121	CCCAGACTGCCCCCTGCCTGTTGCCCTGAGCCACCTACTGCTCCAGATCGTGCAACT	180
Qy	61	AlaValAlaThrAlaSerArgLeuGlyProTyrValLeuLeuGluProGluGluGlyGly	80
Db	181	GCTGTGGCCACTGCCTCCCGTCTTGGGCCCTATGTCTCTCTGGAGCCCGAGGAGGGCGGG	240
Qy	81	ArgAlaTyrGlnAlaLeuHisCysProThrGlyThrGluTyrThrCysLysValTyrPro	100
Db	241	CGGGCCTACCAGGCCCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCC	300
Qy	101	ValGlnGluAlaLeuAlaValLeuGluProTyrAlaArgLeuProProHisLysHisVal	120
Db	301	GTCCAGGAAGCCCTGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCGCAAGCATGTG	360
Qy	121	AlaArgProThrGluValLeuAlaGlyThrGlnLeuLeuTyrAlaPhePheThrArgThr	140
Db	361	GCTCGGCCCACTGAGGTCTGGCTGGTACCCAGCTCCTCTACGCCTTTTCTACTCGGACC	420
Qy	141	HisGlyAspMetHisSerLeuValArgSerArgHisArgIleProGluProGluAlaAla	160
Db	421	CATGGGGACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCC	480
Qy	161	ValLeuPheArgGlnMetAlaThrAlaLeuAlaHisCysHisGlnHisGlyLeuValLeu	180
Db	481	GTGCTCTTCCGCCAGATGGCCACCGCCCTGGCGCACTGTCAACAGCACGGTCTGGTCCTG	540
Qy	181	ArgAspLeuLysLeuCysArgPheValPheAlaAspArgGluArgLysLysLeuValLeu	200
Db	541	CGTGATCTCAAGCTGTGTGCTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTG	600
Qy	201	GluAsnLeuGluAspSerCysValLeuThrGlyProAspAspSerLeuTrpAspLysHis	220
Db	601	GAGAACCTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCTGTGGGACAAGCAC	660
Qy	221	AlaCysProAlaTyrValGlyProGluIleLeuSerSerArgAlaSerTyrSerGlyLys	240
Db	661	GCGTGCCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAG	720
Qy	241	AlaAlaAspValTrpSerLeuGlyValAlaLeuPheThrMetLeuAlaGlyHisTyrPro	260
Db	721	GCAGCCGATGTCTGGAGCCTGGGCGTGGCGCTCTTACCATGCTGGCCGGCCACTACCCC	780
Qy	261	PheGlnAspSerGluProValLeuLeuPheGlyLysIleArgArgGlyAlaTyrAlaLeu	280

```
Db      781  |||||TTCCAGGACTCGGAGCCTGTCCTGCTCTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTG 840
Qy      281  ProAlaGlyLeuSerAlaProAlaArgCysLeuValArgCysLeuLeuArgArgGluPro 300
Db      841  |||||CCTGCAGGCCTCTCGGCCCTGCCCCGCTGTCTGGTTCGCTGCCTCCTTCGTCGGGAGCCA 900
Qy      301  AlaGluArgLeuThrAlaThrGlyIleLeuLeuHisProTrpLeuArgGlnAspProMet 320
Db      901  |||||GCTGAACGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATG 960
Qy      321  ProLeuAlaProThrArgSerHisLeuTrpGluAlaAlaGlnValValProAspGlyLeu 340
Db      961  |||||CCCTTAGCCCCAACCCGATCCCATCTCTGGGAGGCTGCCAGGTGGTCCCTGATGGACTG 1020
Qy      341  GlyLeuAspGluAlaArgGluGluGluGlyAspArgGluValValLeuTyrGly 358
Db      1021 |||||GGGCTGGACGAAGCCAGGGAAGAGGGAGACAGAGAAGTGGTTCTGTATGGC 1074
<!--EndFragment-->
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SCORE Search Results Details for Application 10527708 and Search Result 20071114_121637_us-10-527-708-1.rag.

Score Home	Retrieve Application	SCORE System	SCORE	Comments /
Page	List	Overview	FAQ	Suggestions

This page gives you Search Results detail for the Application 10527708 and Search Result 20071114_121637_us-10-527-708-1.rag.

[Go Back to previous page](#)

GenCore version 6.2.1
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OM protein - protein search, using sw model

Run on: November 14, 2007, 13:28:46 ; Search time 99 Seconds
(without alignments)
1769.509 Million cell updates/sec

Title: US-10-527-708-1
Perfect score: 1891
Sequence: 1 MRATPLAAPAGSLSRKKRLE.....GLGLDEAREEEGDREVVLYG 358

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2782304 seqs, 489333398 residues

Total number of hits satisfying chosen parameters: 2782304

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_200701:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*
- 10: geneseqp2006s:*
- 11: geneseqp2007s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Length	DB	ID	Description
	Score	Match				
1	1891	100.0	358	4	AAU03509	Aau03509 Human pro
2	1891	100.0	358	8	ADN02195	Adn02195 Human NIP
3	1891	100.0	358	8	ADN02178	Adn02178 Human NIP
4	1891	100.0	358	10	AEL00976	Ael00976 Human pro
5	1888	99.8	358	4	AAB20326	Aab20326 Human pro
6	1888	99.8	358	4	AAM38908	Aam38908 Human pol
7	1888	99.8	358	8	ADN02187	Adn02187 Human NIP
8	1888	99.8	358	8	ADN02191	Adn02191 Human NIP
9	1888	99.8	358	8	ADN02193	Adn02193 Human NIP
10	1888	99.8	393	4	AAM40694	Aam40694 Human pol
11	1887	99.8	358	9	ADZ17680	Adz17680 Human h25
12	1887	99.8	358	10	AEG58959	Aeg58959 Human ser
13	1887	99.8	358	10	AEH13313	Aeh13313 Human ser
14	1887	99.8	398	8	ADX66648	Adx66648 Plant ful
15	1887	99.8	404	8	ADX91164	Adx91164 Plant ful
16	1884	99.6	358	7	ADC59337	Adc59337 Human cel
17	1884	99.6	358	8	ADM72653	Adm72653 Human TAS
18	1884	99.6	358	8	ADM72235	Adm72235 Human TAS
19	1884	99.6	358	8	ADN02183	Adn02183 Human NIP
20	1884	99.6	358	8	ABM82187	Abm82187 Tumour-as
21	1884	99.6	358	9	ADZ17686	Adz17686 Human h25
22	1884	99.6	358	9	AEA04464	Aea04464 Human pro
23	1884	99.6	358	10	AEG58965	Aeg58965 Human ser
24	1884	99.6	358	10	AEH13319	Aeh13319 Human pro
25	1880	99.4	358	8	ADN02185	Adn02185 Human NIP
26	1874	99.1	360	5	ABB80976	Abb80976 Human tri
27	1874	99.1	360	8	ADN02197	Adn02197 Human NIP
28	1874	99.1	360	10	AEG58987	Aeg58987 Human SKI
29	1874	99.1	360	10	AEH13341	Aeh13341 Human SKI
30	1862	98.5	360	7	ADJ70383	Adj70383 Human hea
31	1679	88.8	360	3	AAY69157	Aay69157 PeptideA
32	1679	88.8	360	9	ADZ17689	Adz17689 Human h25
33	1679	88.8	360	10	AEG58968	Aeg58968 Human JJ5
34	1679	88.8	360	10	AEH13322	Aeh13322 Human JJ5
35	1586.5	83.9	323	4	AAB85791	Aab85791 Human kin
36	1586.5	83.9	323	8	ADN02189	Adn02189 Human NIP
37	1337	70.7	255	10	AEL01353	Ael01353 Human pro
38	1327.5	70.2	349	7	ADC59335	Adc59335 Rat cell
39	1327.5	70.2	349	10	AEG58988	Aeg58988 Rat NIPK,
40	1327.5	70.2	349	10	AEH13342	Aeh13342 Rat neuro
41	1102	58.3	233	3	AAB43657	Aab43657 Human can
42	1102	58.3	233	9	ADZ17688	Adz17688 Human h25
43	1102	58.3	233	10	AEG58967	Aeg58967 Human ser
44	1102	58.3	233	10	AEH13321	Aeh13321 Human pro
45	1101	58.2	278	5	ABB06093	Abb06093 Human NS

ALIGNMENTS

RESULT 1

AAU03509

ID AAU03509 standard; protein; 358 AA.

XX

AC AAU03509;

XX
 DT 12-SEP-2001 (first entry)
 XX
 DE Human protein kinase #9.
 XX
 KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;
 KW metabolic disorder; immune related disease; neurological disorder;
 KW neurodegenerative disorder; inflammatory disorder; infectious disease;
 KW reproductive disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200138503-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 22-NOV-2000; 2000WO-US032085.
 XX
 PR 24-NOV-1999; 99US-0167482P.
 XX
 PA (SUGE-) SUGEN INC.
 XX
 PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;
 PI Flanagan P, Clary D;
 XX
 DR WPI; 2001-343950/36.
 DR N-PSDB; AAS06709.
 XX
 PT Nucleic acids encoding human kinase polypeptides, useful for preventing
 PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and
 PT neuronal-associated diseases, and microbial infections.
 XX
 PS Claim 7; Fig 2; 433pp; English.
 XX
 CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel
 CC protein kinases have been identified as members of the tyrosine or
 CC serine/threonine kinase (PTK and STK) families. The polynucleotides
 CC encoding protein kinases and the polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate kinase expression. For example, they may be used to treat
 CC cancers (especially cancers of haematopoietic origin), cardiovascular
 CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
 CC immune related diseases (e.g. rheumatoid arthritis), neurological
 CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.
 CC Parkinson's disease), inflammatory disorders (e.g. asthma), infectious
 CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).
 CC Additionally, polynucleotides encoding protein kinases may be used for
 CC gene therapy and as DNA probes in diagnostic assays. The protein kinase
 CC polypeptides may be used as antigens in the production of antibodies
 CC against the protein kinases and in assays to identify modulators of
 CC protein kinase expression and activity
 XX
 SQ Sequence 358 AA;

Query Match 100.0%; Score 1891; DB 4; Length 358;
 Best Local Similarity 100.0%; Pred. No. 1.1e-175;
 Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGQPRLPPCLLPLSPPTAPDRAT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGQPRLPPCLLPLSPPTAPDRAT 60

```

Qy      61 AVATASRLGPYVLLPEEEGGRAYQALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV 120
      |||
Db      61 AVATASRLGPYVLLPEEEGGRAYQALHCPTGTEYTCKVYPVQEALAVLEPYARLPPHKHV 120

Qy     121 ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPPEAAVLFRQMATALAHCHQHGLVL 180
      |||
Db     121 ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPPEAAVLFRQMATALAHCHQHGLVL 180

Qy     181 RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSKG 240
      |||
Db     181 RDLKLCRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPEILSSRASYSKG 240

Qy     241 AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP 300
      |||
Db     241 AADVWSLGVALFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP 300

Qy     301 AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG 358
      |||
Db     301 AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG 358

```

RESULT 2

ADN02195

ID ADN02195 standard; protein; 358 AA.

XX

AC ADN02195;

XX

DT 17-JUN-2004 (first entry)

XX

DE Human NIPK related protein, SEQ ID 18.

XX

KW Nootropic; neuroprotective; cytostatic; antirheumatic; antiarthritic;
 KW neurodegenerative disease; Neuronal cell death Inducible Putative Kinase;
 KW NIPK; enzyme; human.

XX

OS Homo sapiens.

XX

PN WO2004024920-A1.

XX

PD 25-MAR-2004.

XX

PF 11-SEP-2003; 2003WO-JP011631.

XX

PR 13-SEP-2002; 2002JP-00269091.

XX

PA (TAKE) TAKEDA CHEM IND LTD.

XX

PI Matsui H, Watanabe T;

XX

DR WPI; 2004-270046/25.

DR N-PSDB; ADN02194.

XX

PT Preventives or remedies for neurodegenerative diseases e.g. Alzheimer's
 PT disease containing inhibitors of NIPK and its gene expression, with
 PT promoters in treating cancer and rheumatoid arthritis.

XX

PS Disclosure; SEQ ID NO 18; 125pp; Japanese.

XX

CC The present invention relates to preventives or remedies for
 CC neurodegenerative diseases, which contain compounds or their salts